Identification of the predominant oral microbiome in pericoronitis

ABSTRACT

Accumulation of mixed oral microflora appears to be one of the contributing factors to pericoronitis, an inflammation of the oral soft tissues surrounding the crown of a partially erupted, or impacted mandibular third molars. This study was aimed to identify the predominant infectious bacteria related to pericoronitis and their coexistence with other bacterial species at the infection site. Plaque from pericoronal pockets of lower wisdom teeth of 25 patients that have been diagnosed with pericoronitis were sampled and subjected to a standard microbiological procedure for identification of bacterial species including cultivation on enriched agar plates, biochemical profiling and 16s rRNA PCR analysis. A total of 97 microorganisms were isolated and identified from the cultured samples and 94.73% were Gram-positive bacteria; with the highest incidence of Streptococcus gordonii, Streptococcus mitis, and Streptococcus anginosus. This study also revealed that facultative anaerobes were the predominant group causing pericoronitis (89%). The high occurence of multi-strain bacteria ranging from facultative anaerobic to aerobic bacteria display the importance of their infection networks in pericoronitis. Knowledge gained from this study increases our understanding on the role of different pathogens in pericoronitis and provides new insight into the clinical management of patients and in the prevention of its recurrence.

Keyword: Pericoronitis; Oral bacteria; Mandibular third molar